

## 1 Supplementary materials

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### 3 Table 1A. Lectin specificities and buffer requirements.

Lectin	Preferred specificity	sugar	Supplier	Binding buffer
Concanavalin A (Con A)	$\alpha$ Man, $\alpha$ Glc		Vector Laboratories, Inc., Newark, CA, USA	TBS/0.05% Tween pH 6.3, 1 mM Ca <sup>2+</sup> , 1 mM MnCl <sub>2</sub>
Sambucus nigra lectin (SNA)	Neu5Ac		Vector Laboratories, Inc., Newark, CA, USA	TBS/0.05% Tween pH 5.5
Ricinus communis lectin I (RCA I)	Gal		Vector Laboratories, Inc., Newark, CA, USA	TBS/0.05% Tween pH 7.4
Aleuria aurantia lectin (AAL)	Fuc		Vector Laboratories, Inc., Newark, CA, USA	TBS/0.05% Tween pH 9.0

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18 **Table 2A. Peptides matching the vitellogenin II sequence identified after in-gel tryptic digestion**  
 19 **of yolkin 3 via LC-MS.**

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<b>Protein 1:</b>		Vitellogenin-2 OS=Gallus gallus OX=9031 GN=VTG2 PE=1 SV=1									
<b>Accession:</b>		VIT2_CHICK					<b>Score:</b>		1099,12		
<b>Database:</b>		SwissProt					<b>MW [kDa]:</b>		204,70		
<b>Seq. Coverage [%]:</b>		9,70 %					<b>pI:</b>		9,23		
<b>Modification(s):</b>		Carbamidomethyl, Oxidation									
Cmpd	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification	
570	6	542.7625	-2.56	2	17.5	27.0	1	1579-1587	KARCSVSYNKI	Carbamidomethyl: 3	
1314	2	429.1936	-2.55	2	21.1	36.6	0	1581-1587	RCSVSYNKI	Carbamidomethyl: 1	
2726	20	489.7839	-1.35	2	27.3	46.0	1	1588-1595	KIKTRNEV/KF		
974	17	445.7314	-2.51	2	19.5	69.5	0	1624-1632	K SAGEATNLKA		
4656	2	715.4102	8.47	2	35.4	22.4	1	1624-1637	K SAGEATNLKAINIKI		
2280	4	888.9399	1.54	2	25.3	63.4	0	1638-1653	KIGSHEDMHPVNGQVK L	Oxidation: 8	
3858	2	587.6317	3.16	3	32.0	32.6	0	1638-1653	KIGSHEDMHPVNGQVK L		
18232	11	737.4139	4.80	2	101.3	46.6	0	1702-1714	KTTTIQVPLWMAGKT	Oxidation: 10	
11932	21	729.4167	5.22	2	66.7	54.8	0	1702-1714	KTTTIQVPLWMAGKT		
5326	13	1069.9330	0.51	2	38.2	95.1	1	1715-1731	KTCGICGKY DAECEQEY R.M	Carbamidomethyl: 2, 5, 12	
4663	26	681.7656	-2.07	2	35.4	89.0	0	1722-1731	KY DAECEQEY R.M	Carbamidomethyl: 5	
5688	1	1126.9827	-0.28	2	39.7	55.9	1	1722-1739	KY DAECEQEY RMPNGYLAK.N	Carbamidomethyl: 5; Oxidation: 11	
9173	45	986.9796	9.33	2	54.3	104.4	0	1740-1756	KNAVSEFGHSWLEAFQR.G	Carbamidomethyl: 16	
2872	30	425.7543	-2.22	2	27.9	40.8	1	1764-1770	R.SFVKLEKT		
5232	30	509.2815	-1.70	2	37.8	71.1	0	1771-1780	KTVQLAGVDSK.C		
5892	33	562.7729	-1.75	2	40.6	53.6	0	1781-1789	KCY STEPVLR.C	Carbamidomethyl: 1	
7642	9	1166.0686	0.60	2	47.8	80.7	0	1799-1820	K TTPVTVGRHCLPADSANSITDK	Carbamidomethyl: 10	
5	2	478.7288	-0.24	2	12.6	25.3	1	1821-1827	KQMKY DQK.S	Oxidation: 2	
4336	3	1080.7345	-2.80	3	34.1	22.5	1	1824-1850	KY DQKSEDMQDITVDAHTTCSCENE	Carbamidomethyl: 18, 20, 25	

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26 **Table 3A. Peptides matching the vitellogenin I sequence identified after in-gel tryptic digestion of**  
 27 **yolkin 3 via LC-MS.**

<b>Protein 2:</b>		Vitellogenin-1 OS=Gallus gallus OX=9031 GN=VTG1 PE=1 SV=1								
<b>Accession:</b>		VIT1_CHICK				<b>Score:</b>		795,61		
<b>Database:</b>		SwissProt				<b>MW [kDa]:</b>		210,50		
<b>Seq. Coverage [%]:</b>		6,60 %				<b>pI:</b>		9,16		
						<b>No. of Peptides:</b>		12		
<b>Modification(s):</b>		Carbamidomethyl, Oxidation								
Cmpd.	No. of Cmpds.	m/z meas.	$\Delta$ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
3023	11	872.3934	0.34	2	28.5	72.7	0	1664-1678	K.SCNVVVAQDCTEHPKF	Carbamidomethyl: 2, 10
378	1	535.2901	-1.83	2	16.4	36.2	1	1685-1693	R.KVDHQSLRSRE	
6233	13	638.8881	5.18	2	42.0	55.6	0	1745-1756	K.TVIVEARIHGLKN	
71	7	532.2399	-0.63	3	13.8	61.2	2	1775-1788	R.GKTCGVCGNNDREKH	Carbamidomethyl: 4, 7
663	6	576.7286	-1.79	2	17.9	52.1	0	1777-1786	K.TCGVCGNNDRE.E	Carbamidomethyl: 2, 5
391	6	705.2992	1.06	2	16.5	67.5	1	1777-1788	K.TCGVCGNNDREKH	Carbamidomethyl: 2, 5
1039	3	624.8104	-1.53	2	19.8	54.9	0	1789-1798	K.HNELMPNHL	Oxidation: 6
7141	17	836.4064	-1.39	3	45.7	71.3	1	1830-1851	K.LNRNPTDGEESTCYSDVPLK	Carbamidomethyl: 14
691	6	649.2816	-1.96	2	18.1	67.0	1	1852-1861	R.QMKDCTPEKT	Carbamidomethyl: 1, 5; Oxidation: 2
2023	16	431.7018	-1.40	2	24.2	34.2	0	1855-1861	K.DCTPEKT	Carbamidomethyl: 2
9682	13	637.3512	4.08	2	56.4	83.6	0	1874-1884	K.ATAVSLEWQRS	
11517	5	1246.4731	0.34	2	64.7	32.0	0	1890-1912	K.SASEDMVESVDAIDICTCTGDCS	Carbamidomethyl: 16, 18, 22

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40 **Table 4A. Summary table with parameters characterizing yolkin thermal stability.**

41 The 330/350 nm ratio is represented as IPs corresponding to the T<sub>m</sub> values and an onset of unfolding as  
 42 ON. Aggregation is shown as the IP corresponding to the inflection point of the scattering. In addition,  
 43 the slope of aggregation, temperature onset of aggregation, and average aggregation values are recorded  
 44 and presented in the table.

		Annotations	Ratio $\lambda$						Scattering $\lambda$							
			IP #1		IP #2		ON		IP #1		Slope at IP #1		ON		ScatteringAverage	
Exclude	^	Sample ID	$\varnothing$	$\sigma$	$\varnothing$	$\sigma$	$\varnothing$	$\sigma$	$\varnothing$	$\sigma$	$\varnothing$	$\sigma$	$\varnothing$	$\sigma$	$\varnothing$	$\sigma$
Excluded		yolkin 12	47,64	0,10	73,29	0,09	20,00	0,00	N/A	N/A	N/A	N/A	N/A	N/A	5,1	1,8
Excluded		yolkin 13	46,76	0,89	73,43	0,16	20,00	0,00	N/A	N/A	N/A	N/A	N/A	N/A	1,5	7,5
Excluded		yolkin 14	47,47	0,16	72,46	0,06	20,00	0,00	75,69	2,79	3,87	1,22	69,36	2,63	35,9	4,7
Excluded		yolkin 15	48,34	0,62	72,57	0,03	20,00	0,00	75,58	0,16	4,33	0,59	72,40	0,43	23,5	6,8
Excluded		lgY	48,35	0,11	72,35	0,08	40,80	0,15	74,22	0,00	5,74	0,45	59,69	0,18	46,9	0,7
Excluded		yolkin 3	N/A	N/A	71,17	0,10	57,71	0,49	79,43	0,20	3,39	0,18	76,45	0,00	17,3	1,6

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